

AMENDMENTS TO THE SPECIFICATION:

The following amendments to the specification were previously presented in Applicants' Amendment mailed January 19, 2006; however, as noted by the Examiner in the Office Action mailed April 5th, 2006, there were informalities in the format of some of the amendments. Accordingly, corrected versions of these amendments are presented below.

Please enter the sequence listing filed on January 20th, 2006 into the specification.

Please amend the title beginning on line 1 of page 1 as follows:

**STRUCTURE OF A GLUCOCORTICOID RECEPTOR LIGAND-BINDING DOMAIN
COMPRISING AN EXPANDED BINDING POCKET AND
METHODS EMPLOYING SAME
METHODS FOR IDENTIFYING GLUCOCORTICOID RECEPTOR MODULATORS**

Please amend the paragraph beginning on line 22 of 114 as follows:

Between mammalian species, e.g. human and mouse, homologs have substantial sequence similarity, i.e. at least 75% sequence identity between nucleotide sequences. Sequence similarity is calculated based on a reference sequence, which can be a subset of a larger sequence, such as a conserved motif, coding region, flanking region, etc. A reference sequence will usually be at least about 18 nt long, more usually at least about 30 nt long, and can extend to the complete sequence that is being compared. Algorithms for sequence analysis are known in the art, such as BLAST, described in Altschul et al., (1990) *J. Mol. Biol.* 215:403-10. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (www.ncbi.nlm.nih.gov/ <http://www.ncbi.nlm.nih.gov/>).